

5/20

#10

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RAW SEQUENCE LISTING

DATE: 05/23/2002

PATENT APPLICATION: US/09/989,975

TIME: 17:24:59

Input Set : A:\13558-004001.TXT

Output Set: N:\CRF3\05232002\I989975.raw

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4 <110> APPLICANT: Abe, Hiroko
5     Shimma, Yoh-ichi
6     Jigami, Yoshifumi
8 <120> TITLE OF INVENTION: NUCLEIC ACIDS, EXPRESSION VECTORS AND
9     HOST CELLS FOR MAKING CHIMERIC NUCLEIC ACIDS AND METHODS FOR
10    PRODUCING IMMOBILIZED POLYPEPTIDES
13 <130> FILE REFERENCE: 13558-004001
15 <140> CURRENT APPLICATION NUMBER: 09/989,975
16 <141> CURRENT FILING DATE: 2001-11-21
18 <150> PRIOR APPLICATION NUMBER: JP 2001-190524
19 <151> PRIOR FILING DATE: 2001-06-22
21 <150> PRIOR APPLICATION NUMBER: JP 2000-354396
22 <151> PRIOR FILING DATE: 2000-11-21
24 <160> NUMBER OF SEQ ID NOS: 14
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 341
30 <212> TYPE: PRT
31 <213> ORGANISM: Saccharomyces cerevisiae
33 <400> SEQUENCE: 1
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35 1             5             10             15
36 Leu Ala Ala Tyr Ala Pro Lys Asp Pro Trp Ser Thr Leu Thr Pro Ser
37             20             25             30
38 Ala Thr Tyr Lys Gly Gly Ile Thr Asp Tyr Ser Ser Thr Phe Gly Ile
39             35             40             45
40 Ala Val Glu Pro Ile Ala Thr Thr Ala Ser Ser Lys Ala Lys Arg Ala
41             50             55             60
42 Ala Ala Ile Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr Lys
43 65             70             75             80
44 Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala
45             85             90             95
46 Thr Thr Lys Thr Lys Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln
47             100            105            110
48 Ile Gln Ala Thr Thr Lys Thr Thr Ser Ala Lys Thr Thr Ala Ala Ala
49             115            120            125
50 Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr Lys Thr Lys
51             130            135            140
52 Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr
53 145            150            155            160
54 Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln
55             165            170            175
56 Ala Thr Thr Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly

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57          180          185          190
58 Gln Ile Gln Ala Thr Thr Asn Thr Thr Val Ala Pro Val Ser Gln Ile
59          195          200          205
60 Thr Asp Gly Gln Ile Gln Ala Thr Thr Leu Thr Ser Ala Thr Ile Ile
61          210          215          220
62 Pro Ser Pro Ala Pro Ala Pro Ile Thr Asn Gly Thr Asp Pro Val Thr
63 225          230          235          240
64 Ala Glu Thr Cys Lys Ser Ser Gly Thr Leu Glu Met Asn Leu Lys Gly
65          245          250          255
66 Gly Ile Leu Thr Asp Gly Lys Gly Arg Ile Gly Ser Ile Val Ala Asn
67          260          265          270
68 Arg Gln Phe Gln Phe Asp Gly Pro Pro Pro Gln Ala Gly Ala Ile Tyr
69          275          280          285
70 Ala Ala Gly Trp Ser Ile Thr Pro Glu Gly Asn Leu Ala Ile Gly Asp
71          290          295          300
72 Gln Asp Thr Phe Tyr Gln Cys Leu Ser Gly Asn Phe Tyr Asn Leu Tyr
73 305          310          315          320
74 Asp Glu His Ile Gly Thr Gln Cys Asn Ala Val His Leu Gln Ala Ile
75          325          330          335
76 Asp Leu Leu Asn Cys
77          340
79 <210> SEQ ID NO: 2
80 <211> LENGTH: 413
81 <212> TYPE: PRT
82 <213> ORGANISM: Saccharomyces cerevisiae
84 <400> SEQUENCE: 2
85 Met Gln Tyr Lys Lys Thr Leu Val Ala Ser Ala Leu Ala Ala Thr Thr
86 1          5          10          15
87 Leu Ala Ala Tyr Ala Pro Ser Glu Pro Trp Ser Thr Leu Thr Pro Thr
88          20          25          30
89 Ala Thr Tyr Ser Gly Gly Val Thr Asp Tyr Ala Ser Thr Phe Gly Ile
90          35          40          45
91 Ala Val Gln Pro Ile Ser Thr Thr Ser Ser Ala Ser Ser Ala Ala Thr
92          50          55          60
93 Thr Ala Ser Ser Lys Ala Lys Arg Ala Ala Ser Gln Ile Gly Asp Gly
94 65          70          75          80
95 Gln Val Gln Ala Ala Thr Thr Thr Ala Ser Val Ser Thr Lys Ser Thr
96          85          90          95
97 Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr
98          100          105          110
99 Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln
100          115          120          125
101 Ala Thr Thr Lys Thr Thr Ser Ala Lys Thr Thr Ala Ala Ala Val Ser
102          130          135          140
103 Gln Ile Ser Asp Gly Gln Ile Gln Ala Thr Thr Thr Thr Leu Ala Pro
104 145          150          155          160
105 Lys Ser Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln
106          165          170          175
107 Ala Thr Thr Thr Thr Leu Ala Pro Lys Ser Thr Ala Ala Ala Val Ser

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108          180          185          190
109 Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Thr Lys Thr Thr Ala Ala
110          195          200          205
111 Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Thr Lys Thr
112          210          215          220
113 Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr
114 225          230          235          240
115 Thr Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val
116          245          250          255
117 Gln Ala Thr Thr Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Thr Asp
118          260          265          270
119 Gly Gln Val Gln Ala Thr Thr Lys Thr Thr Gln Ala Ala Ser Gln Val
120          275          280          285
121 Ser Asp Gly Gln Val Gln Ala Thr Thr Ala Thr Ser Ala Ser Ala Ala
122          290          295          300
123 Ala Thr Ser Thr Asp Pro Val Asp Ala Val Ser Cys Lys Thr Ser Gly
124 305          310          315          320
125 Thr Leu Glu Met Asn Leu Lys Gly Gly Ile Leu Thr Asp Gly Lys Gly
126          325          330          335
127 Arg Ile Gly Ser Ile Val Ala Asn Arg Gln Phe Gln Phe Asp Gly Pro
128          340          345          350
129 Pro Pro Gln Ala Gly Ala Ile Tyr Ala Ala Gly Trp Ser Ile Thr Pro
130          355          360          365
131 Asp Gly Asn Leu Ala Ile Gly Asp Asn Asp Val Phe Tyr Gln Cys Leu
132          370          375          380
133 Ser Gly Thr Phe Tyr Asn Leu Tyr Asp Glu His Ile Gly Ser Gln Cys
134 385          390          395          400
135 Thr Pro Val His Leu Glu Ala Ile Asp Leu Ile Asp Cys
136          405          410
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139 <211> LENGTH: 44
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Synthetic primer
146 <400> SEQUENCE: 3
147 ggggggagct catgcaatac aaaaaatcat tagttgcctc cgcc
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 31
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Synthetic primer
157 <400> SEQUENCE: 4
158 ccccgcggc cgcacagtgc aaatcgatag c
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 35
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence

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44

31

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165 <220> FEATURE:
166 <223> OTHER INFORMATION: Synthetic primer
168 <400> SEQUENCE: 5
169 ggggggcggc cgcataccca tacgatgttc ctgac 35
171 <210> SEQ ID NO: 6
172 <211> LENGTH: 47
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Synthetic primer
179 <400> SEQUENCE: 6
180 gggggccggg ctaggatgat ggtttcaaaa gattttgaat atgatcc 47
182 <210> SEQ ID NO: 7
183 <211> LENGTH: 35
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Synthetic primer
190 <400> SEQUENCE: 7
191 cccgtcgaca atcctatctg cgtgtgtctc aagac 35
193 <210> SEQ ID NO: 8
194 <211> LENGTH: 35
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Synthetic primer
201 <400> SEQUENCE: 8
202 cccctcgagt caggtgaacc aagccgctat gccgc 35
204 <210> SEQ ID NO: 9
205 <211> LENGTH: 39
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Synthetic primer
212 <400> SEQUENCE: 9
213 ggggggtcga cagcaatata ttccgagttc catctccgc 39
215 <210> SEQ ID NO: 10
216 <211> LENGTH: 42
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Synthetic primer
223 <400> SEQUENCE: 10
224 ggggggtcga gctactcacg gaattttttc cagttttttg gc 42
226 <210> SEQ ID NO: 11
227 <211> LENGTH: 38
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:

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232 <223> OTHER INFORMATION: Synthetic primer
234 <400> SEQUENCE: 11
235 ggggggagct catgcaatac aaaaagactt tggttgcc 38
237 <210> SEQ ID NO: 12
238 <211> LENGTH: 68
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Synthetic primer
245 <400> SEQUENCE: 12
246 ccccgcggc cgccttgta tgcatacct ttagtcaca gtctatcaaa tcgatagctt 60
247 ccaagtgg 68
249 <210> SEQ ID NO: 13
250 <211> LENGTH: 49
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Synthetic primer
257 <400> SEQUENCE: 13
258 ggggggcggc cgcaaagat gcgcttatac gatcaagcaa tgtaaacag 49
260 <210> SEQ ID NO: 14
261 <211> LENGTH: 38
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Synthetic primer
268 <400> SEQUENCE: 14
269 gggggcccg gctagctttg ttogtgtcta gaattttc 38

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VERIFICATION SUMMARY

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Input Set : A:\13558-004001.TXT

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